

5. A purified antibody which binds specifically to any of the amino acid sequence of Claim 3.

6. A purified antibody which binds to an amino acid sequence which is present only in the alternative splice variant depicted in the amino acid of Claim 3, but is not present in the original amino sequence.
7. A purified antibody which binds to an amino acid sequence present in the original amino acid sequence, which amino acid sequence is not present in the amino acid sequence of Claim 3.
8. An expression vector comprising any one of the nucleic acid sequences of Claim 1 and control elements for the expression of the nucleic acid sequence in a suitable host.
9. An expression vector comprising any one of the nucleic acid sequences of Claim 2, and control elements for the expression of the nucleic acid sequences in a suitable host.
10. A host cell transfected by the expression vector of Claim 8.
11. A host cell transfected by the expression vector of Claim 9.
12. A pharmaceutical composition comprising a pharmaceutically acceptable carrier and as an active ingredient an agent selected from the group consisting of:
  - (i) the expression vector of Claim 8; and
  - (ii) any one of the amino acid sequences of Claim 3.
13. A pharmaceutical composition according to Claim 12, for treatment of diseases which can be ameliorated or cured by raising the level of any one of the amino acid sequences of Claim 3.
14. A pharmaceutical composition comprising a pharmaceutically acceptable carrier and as an active ingredient an agent selected from the group consisting of:
  - (i) any one of the nucleic acid sequences of Claim 2;
  - (ii) the expression vector of Claim 9; and
  - (iii) the purified antibody of Claim 5.
15. A pharmaceutical composition according to Claim 14, for treatment of diseases which can be ameliorated or cured by decreasing the level of any one of the amino acid sequences of Claim 3.

16. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

- (i) the nucleic acid sequence depicted in any one of NV\_1-5525;
- (ii) nucleic acid sequences having at least 90% identity with the  
5 sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and
- (iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in  
10 the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

17. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

- (i) the nucleic acid sequence depicted in any one of NV\_5526-6579;
- 15 (ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and
- (iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment  
20 contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

18. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

- 25 (i) the nucleic acid sequence depicted in any one of NV\_6580-6781;
- (ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

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(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

5 19. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

(i) the nucleic acid sequence depicted in any one of NV\_6782-7426;

(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original  
10 nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been  
15 varied by alternative splicing.

20 20. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

(i) the nucleic acid sequence depicted in any one of NV\_7427-10085;

(ii) nucleic acid sequences having at least 90% identity with the  
20 sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in  
25 the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

21. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

(i) the nucleic acid sequence depicted in any one of NV\_10086-10386;

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(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

5 (iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

22. An isolated nucleic acid sequence, of an alternative splicing variant, selected  
10 from the group consisting of:

(i) the nucleic acid sequence depicted in any one of NV\_10387-10762;

(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by  
15 alternative splicing; and

(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

20 23. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

(i) the nucleic acid sequence depicted in any one of NV\_10763-11439;

(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original  
25 nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been  
30 varied by alternative splicing.

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24. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

- (a) the nucleic acid sequence depicted in any one of NV\_11440-11463;
- (b) nucleic acid sequences having at least 90% identity with the  
5 sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and
- (c) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in  
10 the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

25. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

- (i) the nucleic acid sequence depicted in any one of NV\_11464-11572;
- 15 (ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and
- (iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment  
20 contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

26. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

- 25 (i) the nucleic acid sequence depicted in any one of NV\_11573-11599;
- (ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

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(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

5 27. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

(i) the nucleic acid sequence depicted in any one of NV\_11600-12505;

(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original  
10 nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been  
15 varied by alternative splicing.

28. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

(i) the nucleic acid sequence depicted in any one of NV\_12506-12648;

(ii) nucleic acid sequences having at least 90% identity with the  
20 sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in  
25 the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

29. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

(i) the nucleic acid sequence depicted in any one of NV\_12649-13504;

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5 (iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

(i) the nucleic acid sequence depicted in any one of NV\_1350-5-14159;

(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

(i) the nucleic acid sequence depicted in any one of NV\_14160-14368;

(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original

25 nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.



(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

5 35. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

(i) the nucleic acid sequence depicted in any one of NV\_15896-17110;

(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original  
10 nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been  
15 varied by alternative splicing.

36. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

(i) the nucleic acid sequence depicted in any one of NV\_17111-18639;

(ii) nucleic acid sequences having at least 90% identity with the  
20 sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in  
25 the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

37. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

(i) the nucleic acid sequence depicted in any one of NV\_18640-19766;

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5 (iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

(i) the nucleic acid sequence depicted in any one of NV\_19767-22843;

(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

20     **39.** An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

(i) the nucleic acid sequence depicted in any one of NV\_22844-23081;

(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original

25 nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

40. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

- (i) the nucleic acid sequence depicted in any one of NV\_23082-27305;
- (ii) nucleic acid sequences having at least 90% identity with the  
5 sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and
- (iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in  
10 the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

41. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

- (i) the nucleic acid sequence depicted in any one of NV\_27306-29408;
- 15 (ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and
- (iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment  
20 contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

42. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

- 25 (i) the nucleic acid sequence depicted in any one of NV\_29409-29485;
- (ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

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(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

5    **43.** An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

        (i) the nucleic acid sequence depicted in any one of NV\_29486-29914;

        (ii) nucleic acid sequences having at least 90% identity with the  
sequence of (i) with the proviso that each sequence is different than the original  
10 nucleic acid sequence from which the sequences of (i) have been varied by  
alternative splicing; and

        (iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment  
contains a sequence which is not present, as a continuous stretch of nucleotides, in  
the original nucleic acid sequence from which the sequences of (i) have been  
15 varied by alternative splicing.

**44.** An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

        (i) the nucleic acid sequence depicted in any one of NV\_29915-30434;

        (ii) nucleic acid sequences having at least 90% identity with the  
20 sequence of (i) with the proviso that each sequence is different than the original  
nucleic acid sequence from which the sequences of (i) have been varied by  
alternative splicing; and

        (iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment  
contains a sequence which is not present, as a continuous stretch of nucleotides, in  
25 the original nucleic acid sequence from which the sequences of (i) have been  
varied by alternative splicing.

**45.** An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

        (i) the nucleic acid sequence depicted in any one of NV\_30435-30575;

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(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

- 5 (iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

46. An isolated nucleic acid sequence, of an alternative splicing variant, selected  
10 from the group consisting of:

- (i) the nucleic acid sequence depicted in any one of NV\_30576-31459;  
(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by  
15 alternative splicing; and

(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

20 47. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

- (i) the nucleic acid sequence depicted in any one of NV\_31460-31753;  
(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original  
25 nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been  
30 varied by alternative splicing.

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48. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

- (i) the nucleic acid sequence depicted in any one of NV\_31754-33145;
- (ii) nucleic acid sequences having at least 90% identity with the  
5 sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and
- (iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in  
10 the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

49. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

- (i) the nucleic acid sequence depicted in any one of NV\_33146-34829;
- 15 (ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and
- (iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment  
20 contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

50. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

- 25 (i) the nucleic acid sequence depicted in any one of NV\_34830-35550;
- (ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

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(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

5    **51.** An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

          (i) the nucleic acid sequence depicted in any one of NV\_35551-35660;

          (ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original  
10 nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

          (iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been  
15 varied by alternative splicing.

**52.** An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

          (i) the nucleic acid sequence depicted in any one of NV\_35661-36150;

          (ii) nucleic acid sequences having at least 90% identity with the  
20 sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

          (iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in  
25 the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

**53.** An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

          (i) the nucleic acid sequence depicted in any one of NV\_36151-37125;

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(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

5 (iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

54. An isolated nucleic acid sequence, of an alternative splicing variant, selected  
10 from the group consisting of:

(i) the nucleic acid sequence depicted in any one of NV\_37126-38380;

(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by  
15 alternative splicing; and

(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

20 55. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

(i) the nucleic acid sequence depicted in any one of NV\_38381-45130;

(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original  
25 nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been  
30 varied by alternative splicing.

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56. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

- (i) the nucleic acid sequence depicted in any one of NV\_45131-46553;
- (ii) nucleic acid sequences having at least 90% identity with the  
5 sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and
- (iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in  
10 the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

57. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

- (i) the nucleic acid sequence depicted in any one of NV\_46554-47029;
- 15 (ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and
- (iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment  
20 contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

58. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:

- 25 (i) the nucleic acid sequence depicted in any one of NV\_47030-48611;
- (ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

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(iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

5    59. A method for detecting a variant nucleic acid sequence in a biological sample, comprising the steps of:

      (a) hybridizing to nucleic acid material of said biological sample any one of the nucleic acid sequences of Claim 1; and

      (b) detecting said hybridization complex;

10    60. A method for determining the level of variant nucleic acid sequences in a biological sample comprising the steps of:

      (a) hybridizing to nucleic acid material of said biological sample any one of the nucleic acid sequences of Claim 1; and

      (b) determining the amount of hybridization complexes and normalizing  
15 said amount to provide the level of the variant nucleic acid sequences in the sample.

      61. A method for determining the ratio between the level of variant of the nucleic acid sequence in a first biological sample and the level of the original sequence from which the variant has been varied by alternative splicing in a second biological sample comprising:

20       (a) determining the level of the variant nucleic acid sequence in the first biological sample according to the method of Claim 60;

      (b) determining the level of the original sequence in the second biological sample; and

      (c) comprising the levels obtained in (a) and (b) to give said ratio.

25    62. A method according to Claim 61, wherein said first and said second biological samples are the same sample.

      63. A method according to Claim 59, wherein the nucleic acid material of said biological sample are mRNA transcripts.

      64. A method according to Claim 59, where the nucleic acid sequence is present  
30 in a nucleic acid chip.

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65. A method for detecting any one of the amino acid sequences of Claim 3 in a biological sample, comprising the steps of:

(a) contacting with said biological sample the antibody of Claim 5, thereby forming an antibody-antigen complex; and

5 (b) detecting said antibody-antigen complex

wherein the presence of said antibody-antigen complex correlates with the presence of the desired amino acid in said biological sample.

66. A method for detecting the level of the amino acid sequence of any one of Claim 3 in a biological sample, comprising the steps of:

10 (a) contacting with said biological sample the antibody of Claim 5, thereby forming an antibody-antigen complex; and

(b) detecting the amount of said antibody-antigen complex and normalizing said amount to provide the level of said amino acid sequence in the sample.

15 67. A method for determining the ratio between the level of any one of the amino acid sequence of Claim 3 present in a first biological sample and the level of the original amino acid sequences from which they were varied by alternative splicing, present in a second biological sample, the method comprising:

(a) determining the level of the amino acid sequences of Claim 3 into a  
20 first sample by the method of Claim 66;

(b) determining the level of the original amino acid sequence in the second sample; and

(c) comparing the level obtained in (a) and (b) to give said ratio.

25 68. A method according to Claim 67, wherein said first and said second biological samples are the same sample.

69. A nucleic acid sequence according to Claim 1, present on a data carrier.

70. A data carrier comprising substantially all the nucleic acid sequences depicted in NV\_1 to NV\_48611.

30 71. A data carrier according to Claim 70, further comprising the amino acid sequences coded by any one of NV\_1 to NV\_48611.

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72. A data carrier according to Claim 71, for use in an analysis of a nucleic acid sequence in which said nucleic acid sequence is compared to any of the sequence present on the data carrier.

73. A software data combination comprising:

- 5        a nucleic acid sequence search and comparison software and data comprising substantially sequences depicted in NV\_1 to NV\_48611; said combination when loaded into a computer can execute in the computer a search where a nucleotide sequence is compared to the sequences comprising said data.

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